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 <141> 2001-01-24  
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 <151> 1998-07-28  
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20 25 30	
aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc	144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe	
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
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Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
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65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
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115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
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Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
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ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gaa gtt gtc      432
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Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu	
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Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
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Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
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Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
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Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
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100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met  
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu  
145 150 155 160

Arg Leu Arg Arg Lys Glu  
165

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<220>  
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<220>  
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 1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80

ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288  
 Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu

165

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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
145 150 155 160

Ser Leu Arg Ser Lys Glu  
165

<210> 37  
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<220>  
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<220>  
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 1 5 10 15  
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30  
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80  
 ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc 288  
 Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160  
 agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu

165

<210> 38  
<211> 166  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
145 150 155 160

Ser Leu Arg Ser Lys Glu  
165

<210> 39  
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<400> 39  
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 1 5 10 15  
  
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30  
  
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
  
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80  
  
 ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc 288  
 Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95  
  
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
  
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160  
  
 agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu

165

<210> 40  
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 <212> PRT  
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<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

Ser Leu Arg Ser Lys Glu  
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 1 5 10 15  
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30  
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80  
 ctc cta gac aaa ttc tac act gaa ctc aac cag cag ctg aat gac ctc 288  
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160  
 agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu

165

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<211> 166  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
1 5 10 15  
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20 25 30  
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45  
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60  
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
65 70 75 80  
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
85 90 95  
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
100 105 110  
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
115 120 125  
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
130 135 140  
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
145 150 155 160  
Ser Leu Arg Ser Lys Glu  
165